_	_	_		Val 5	_						_			_		48
_		_	_	att Ile			_	-	_	_	_	-		_		96
	_		-	gat Asp			_		_	_	_	_			_	144
				cgt Arg	_	_			_	-	_		_			192
	_	_		gga Gly					_		_		_	—		240
_			_	tgg Trp 85	_		-		_	_		-	_	_	-	288
				Ala			_	_	_	_					gct Ala	336
		_	Lys	aaa Lys		-		Thr	_				Asn	_		384
		Val	_	ttc Phe			Asn		_			Asp			gaa Glu	432
_	· Val			a ggt c Gly	_	Ser	_				Cys		_		atg Met 160	480
-		_			Asp	-				e Glr				_	act Thr	528
_		_	_	а Туг			_		1 Met			-		Pro	cac His	576
_		_	y As		_	_		a Arg	_			-	a Asr		gtt Val	624

FIG. 1A

	aac Asn 210			_		_		_				-			gaa Glu	672
	aat Asn				_		_	•		_						720
	tca Ser															768
	gaa Glu															816
	act Thr															864
		Leu	Phe	Asp	Ala	Thr	Gln	Thr	Lys	_	Met	Glu	_	_	gga Gly	912
	Gln					Val									tac Tyr 320	960
	gct Ala				Arg					Phe					-	1008
taa																1011

FIG. 1B

Met	gta Val	gtt Val	aaa Lys	gtt Val 5	ggt	att Ile	aac Asn	ggt Gly	Phe 10	ggt Gly	cgt Arg	atc Ile	ggt Gly	cgt Arg 15	ctt Leu	48
gca Ala	ttc Phe	cgt Arg	cgc Arg 20	atc Ile	caa Gln	aac Asn	gta Val	gaa Glu 25	ggt Gly	gtt Val	gaa Glu	gtt Val	act Thr 30	cgt. Arg	atc Ile	96
aac Asn	gac Asp	ctt Leu 35	aca Thr	gat Asp	cca Pro	aac Asn	atg Met 40	ctt Leu	gca Ala	cac His	ttg Leu	ttg Leu 45	aaa Lys	tat Tyr	gac Asp	144
aca Thr	act Thr 50	caa Gln	ggt Gly	cgt	ttc Phe	gac Asp 55	ggt Gly	act Thr	gtt Val	gaa Glu	gtt Val 60	aaa Lys	gaa Glu	ggt Gly	gga Gly	192
ttc Phe 65	gaa Glu	gtt Val	aac Asn	ggt Gly	caa Gln 70	ttt Phe	gtt Val	aaa Lys	gtt Val	tct Ser 75	gct Ala	gaa Glu	cgc Arg	gaa Glu	cca Pro 80	240
gca Ala	aac Asn	att Ile	gac Asp	tgg Trp 85	gct Ala	act Thr	gat Asp	ggc Gly	gta Val 90	gaa Glu	atc Ile	gtt Val	ctt Leu	gaa Glu 95	gca Ala	288
act Thr	ggt	ttc Phe	ttt Phe 100	gca Ala	tca Ser	aaa Lys	gaa Glu	aaa Lys 105	gct Ala	gga Gly	caa Gln	cac His	atc Ile 110	cat His	gaa Glu	336
aat Asn	ggt	gct Ala 115	aaa Lys	aaa Lys	gtt Val	gtt Val	atc Ile 120	aca Thr	gct Ala	cct Pro	ggt Gly	gga Gly 125	aac Asn	gac Asp	gtt Val	384
aaa Lys	aca Thr 130	gtt Val	gtt Val	ttc Phe	aac Asn	act Thr 135	aac Asn	cac His	gat Asp	atc Ile	ctt Leu 140	gat Asp	gga Gly	act Thr	gaa Glu	432
aca Thr 145	gtt Val	atc Ile	tca Ser	ggt Gly	gct Ala 150	tca Ser	tgt Cys	act Thr	aca Thr	aac Asn 155	tgt Cys	ctt Leu	get Ala	cca Pro	atg Met 160	480
gct Ala	aaa Lys	gct Ala	tta Leu	caa Gln 165	gac	aac Asn	ttt Phe	ggt Gly	gtt Val 170	aaa Lys	caa Gln	ggt Gly	ttg Leu	atg Met 175	act Thr	528
act Thr	atc Ile	cac His	gca Ala 180	TAT	IIII	ggt Gly	Asp	caa Gln 185	Met	Ile	Leu	gac Asp	Gly	Pro	cac His	576
cgt Arg	ggt Gly	ggt Gly 195	gac Asp	ctt Leu	cgt Arg	cgt Arg	gct Ala 200	cgt Arg	gca Ala	ggt Gly	gct Ala	gca Ala 205	aac Asn	atc Ile	gtt Val	624

FIG. 2A

	aac Asn 210			-		_		_							_	672
_	aac Asn				_		_	_		_	•		_			720
	tca Ser	-		_						_			_		_	768
_	gaa Glu	_		_		_		_	_	_		_				816
	act Thr	_	-						_		-					864
		Leu		_	_		Gln			_		Thr	_	_	ggt Gly	912
	Gln	_	•		_	Val				_	Asn	-	_		tac Tyr 320	960
	tca Ser			-	Arg					Phe	_			-	_	1008
taa																1011

FIG. 2B

Met 1	Val	Val	Lys	Val 5	Gly	Ile	aac Asn	ggt Gly	Phe 10	ggt	Arg	Ile	gga Gly	Arg 15	ctt Leu	48
gca Ala	ttc Phe	cgt Arg	cgt Arg 20	att Ile	caa Gln	aac Asn	gtt Val	gaa Glu 25	ggt Gly	gtt Val	gaa [,] Glu	gta Val	act Thr 30	cgt Arg	att Ile	96
aac Asn	gat Asp	ctt Leu 35	act Thr	Aab gac	cca Pro	aat Asn	atg Met 40	ctt Leu	gca Ala	cac His	ttg Leu	ttg Leu 45	aaa Lys	tat Tyr	gat Asp	144
aca Thr	act Thr 50	caa Gln	ggt Gly	cgt Arg	ttc Phe	gac Asp 55	ggt Gly	aca Thr	gtt Val	gaa Glu	gtt Val 60	aaa Lys	gat Asp	ggt Gly	gga Gly	192
ttc Phe 65	gaa Glu	gtt Val	aac Asn	gga Gly	aac Asn 70	ttc Phe	atc Ile	aaa Lys	gtt Val	tct Ser 75	gct Ala	gaa Glu	aaa Lys	gat Asp	cca Pro 80	240
gaa Glu	aac Asn	att	gac Asp	tgg Trp 85	gca Ala	act Thr	gac Asp	ggt Gly	gta Val 90	gaa Glu	atc Ile	gtt Val	ctt Leu	gaa Glu 95	gca Ala	288
act Thr	ggt Gly	ttc Phe	ttt Phe 100	gct Ala	aaa Lys	aaa Lys	gca Ala	gct Ala 105	gct Ala	gaa Glu	aaa Lys	cat His	tta Leu 110	cat His	gct Ala	336
aac Asn	ggt	gct Ala 115	aaa Lys	aaa Lys	gtt Val	gtt Val	atc Ile 120	aca Thr	gct Ala	cct Pro	ggt Gly	gga Gly 125	gat Asp	gat Asp	gtt Val	384
aaa Lys	act Thr 130	Val	gta Val	ttt Phe	aac Asn	aca Thr 135	aac Asn	cat His	gac Asp	att Ile	ctt Leu 140	gac Asp	ggt Gly	aca Thr	gaa Glu	432
act Thr 145	Val	att Ile	tca Ser	ggt	gct Ala 150	tca Ser	tgt Cys	act Thr	act Thr	aac Asn 155	tgt Cys	tta Leu	gct Ala	cca Pro	atg Met 160	480
gct Ala	aaa Lys	gct Ala	ttg Leu	caa Gln 165	Asp	aac Asn	ttt Phe	ggt Gly	gtt Val 170	Lys	caa Gln	ggt Gly	ttg Leu	atg Met 175	aca Thr	528
act Thr	atc Ile	cac His	Ala	tac Tyr	Thr	Gly	qaA	Gln	Met	Ile	Leu	Asp	Gly	Pro	cac His	576
cgt Arg	ggt Gly	ggt Gly 195	. Yeb	ctt Leu	cgt Arg	cgt Arg	gct Ala 200	Arg	gct Ala	ggt Gly	gca Ala	agc Ser 205	aac Asn	att Ile	gtt Val	624

FIG. 3A

					gca Ala					672
					gca Ala					720
					gtt Val					768
					gca Ala 265					816
					tct Ser					864
					act Thr				gga Gly	912
	Gln				tgg Trp					960
			Arg		gag Glu	Phe				1008
taa										1011

FIG. 3B

	gta Val	_		-				_					_			48
	ttc Phe									_				_		96
	gac Asp		_				_		_		_				_	144
	act Thr 50		-	_			_		_	_	_		_			192
	gac Asp	_							_		_	_		_		240
_	caa Gln		_				_		_	_		-			_	288
	ggt Gly			Ala			_	_	_	_					gaa Glu	336
	ggt Gly	_	Lys					Thr	-				_	_	gtg Val	384
	aca Thr 130	Val	_				Asn		_			Asp			gaa Glu	432
	. Val				_	Ser	_				Сув		-		atg Met 160	480
		_			qaA				_	Lys				_	act Thr	528
_				а Туг		Gly	Asp		Met	-		_		Pro	cac His	576
_		_	As]					a Arg	-	-			. Asr		gtt Val	624

FIG. 4A

				-				gca Ala				_			_	672
						_	_	gca Ala		-	_		_			720
								gtt Val				_			_	768
-					-	-		gct Ala 265	_	_		_				816
			-			-		tct Ser	-		_		_			864
		Leu		_	-			act Thr		_		Thr	_	_	gga Gly	912
	Gln		-		_	Val		tgg Trp		_	Asn	_	_			960
					Arg			gag Glu		Phe					Lys	1008
taa																1011

FIG. 4B

_	_	-		Val 5				_				_	_			48
_		_		att Ile	_		-	_		_	_	_	_	_		96
	_			gat Asp			. –		_			_			_	144
•		Gln		cgt Arg					_	_						192
	Glu			gga Gly												240
_			_	tgg Trp 85	_				_							288
				Ala											gct Ala	336
			Lys	aaa Lys	_	_		Thr	_						gtt Val	384
		Val	•				Asn		_			Asp			gaa Glu	432
	. Val				_	Ser	_				Cys				atg Met 160	480
		_			ı Āsp				_	Lye					act Thr	528
			s Gl		r Thi	Gly	Asp	Glr	Met	Va]	Lev	ı Asp	Gly	Pro	cac His	576
	_		y As		_		_	a Arg		-	-		A Asr	_	gtt Val	624

FIG. 5A

Pro			_	_		_				gtt Val			_	672
			_	_	_	_		_	_	cct Pro	_			720
										gat Asp			gta Val	768
_				_		_	_			gat Asp				816
										ggt Gly 285				864
	Leu		_		Gln			_		Thr	_	_	gga Gly	912
				Val				_	Asn	gaa Glu	_			960
			Arg					Phe		aaa Lys			_	1008
taa														1011

FIG. 5B

Met 1	Lys	Lys	Ile	Thr 5	Gly	Ile	Ile	Leu	Leu 10	Leu	Leu	gca Ala	gtc Val	Ile 15	Ile	48
ctg Leu	tct Ser	gca Ala	tgc Cys 20	cag Gln	gca Ala	aac Asn	tac Tyr	gga Gly 25	tcc Ser	ggt Gly	atg Met	gta Val	gtt Val 30	aaa Lys	gtt Val	96
ggt Gly	att Ile	aac Asn 35	ggt Gly	ttc Phe	ggt Gly	cgt Arg	atc Ile 40	gga Gly	cgt Arg	ctt Leu	gca Ala	ttc Phe 45	cgt Arg	cgt Arg	att Ile	144
caa Gln	aat Asn 50	gtt Val	gaa Glu	ggt Gly	gtt Val	gaa Glu 55	gta Val	act Thr	cgt Arg	atc Ile	aac Asn 60	gac Asp	ctt Leu	aca Thr	gat Asp	192
cca Pro 65	aac Asn	atg Met	ctt Leu	gca Ala	cac His 70	ttg Leu	ttg Leu	aaa Lys	tac Tyr	gat Asp 75	aca Thr	act Thr	çaa Gln	gga Gly	cgt Arg 80	240
ttt Phe	gac Asp	gga Gly	act	gtt Val 85	gaa Glu	gtt Val	aaa Lys	gaa Glu	ggt Gly 90	gga Gly	ttt Phe	gaa Glu	gta Val	aac Asn 95	gga Gly	288
aac Asn	ttc Phe	atc Ile	aaa Lys 100	gtt Vaļ	tct Ser	gct Ala	gaa Glu	cgt Arg 105	gat Asp	cca Pro	gaa Glu	aac Asn	atc Ile 110	gac Asp	tgg Trp	336
gca Ala	act Thr	gac Asp 115	ggt Gly	gtt Val	gaa Glu	atc Ile	gtt Val 120	ctg Leu	gaa Glu	gca Ala	ctc Leu	gag Glu 125	ggt Gly	act Thr	gta Val	384
gaa Glu	gtt Val 130	aaa Lys	gat Asp	ggt Gly	gga Gly	ttt Phe 135	gac Asp	gtt Val	aac Asn	gga Gly	aaa Lys 140	ttc Phe	att Ile	aaa Lys	gtt Val	432
tct Ser 145	ALA	gaa Glu	aaa Lys	gat Asp	cca Pro 150	gaa Glu	caa Gln	att Ile	gac Asp	tgg Trp 155	gca Ala	act Thr	gac Asp	ggt Gly	gtt Val 160	480
gaa Glu	atc Ile	gtt Val	ctt Leu	gaa Glu 165	atc Ile	gat Asp	ggt Gly	act Thr	gtt Val 170	gaa Glu	gtt Val	aaa Lys	gaa Glu	ggt Gly 175	gga Gly	528
ttc Phe	gaa Glu	gtt Val	aac Asn 180	Gly	Gln	Phe	gtt Val	Lys	Val	Ser	Ala	Glu	Arg	gaa Glu	cca Pro	576
gca Ala	aac Asn	att Ile 195	Asp	tgg Trp	gct Ala	act Thr	gat Asp 200	ggc Gly	gta Val	gaa Glu	atc Ile	gtt Val 205	ctt Leu	gaa Glu	gca Ala	624

FIG. 6A

1111	agt Ser 210	Phe	Pne	Ala	гЛя	Lys 215	Glu	Ala	Ala	Glu	Lys 220	His	Leu	His	Ala	672
225	ggt Gly	AIG	цув	гув	230	vaı	Ile	Thr	Ala	Pro 235	Gly	Gly	Asn	Asp	Val 240	720
Dy S	aca Thr	val	vai	245	Asn	THE	Asn	His	Asp 250	Ile	Leu	qaA	Gly	Thr 255	Glu	768
IIII	Val	TIE	260	GIY	Ala	Ser	Сув	Thr 265	Thr	Asn	Cya	Leu	Ala 270	Pro		816
gct Ala	Lys Lys	gct Ala 275	ctt Leu	cac His	gat Asp	gca Ala	ttt Phe 280	ggt Gly	atc Ile	caa Gln	aaa Lys	ggt Gly 285	ctt Leu	atg Met	act Thr	864
aca Thr	atc Ile 290	cac His	gct Ala	tat	act Thr	ggt Gly 295	gac Asp	caa Gln	atg Met	atc Ile	ctt Leu 300	gac Asp	gga Gly	cca Pro	cac His	912
cgt Arg 305	ggt Gly	ggt Gly	gac Asp	ctt Leu	cgt Arg 310	cgt Arg	gct Ala	cgt Arg	gct Ala	ggt Gly 315	gct Ala	gca Ala	aac Asn	att Ile	gtt Val 320	960
cct Pro	aac Asn	tca Ser	act Thr	ggt Gly 325	gct Ala	gct Ala	aaa Lys	gct Ala	atc Ile 330	ggt Gly	ctt Leu	gtt Val	atc Ile	cca Pro 335	gaa Glu	1008
ttg Leu	aat Asn	ggt Gly	aaa Lys 340	ctt Leu	gat Asp	ggt Gly	gct Ala	gca Ala 345	caa Gln	cgt Arg	gtt Val	cct Pro	gtt Val 350	cca Pro	act Thr	1056
gga Gly	tca Ser	gta Val 355	act Thr	gag Glu	ttg Leu	gtt Val	gta Val 360	act Thr	ctt Leu	gat Asp	aaa Lys	aac Asn 365	gtt Val	tct Ser	gtt Val	1104
gac Asp	gaa Glu 370	atc	aac Asn	gct Ala	gct Ala	atg Met 375	aaa Lys	gct Ala	gct Ala	tca Ser	aac Asn 380	gac Asp	agt Ser	ttc Phe	ggt Gly	1152
tac Tyr 385	act Thr	gaa Glu	gat Asp	cca Pro	att Ile 390	gtt Val	tct Ser	tca Ser	gat Asp	atc Ile 395	gta Val	ggc Gly	gtg Val	tca Ser	tac Tyr 400	1200
ggt Gly	tca Ser	ttg Leu	ttt Phe	gac Asp 405	gca Ala	act Thr	caa Gln	act Thr	aaa Lys 410	gtt Val	atg Met	gaa Glu	gtt Val	gac Asp 415	gga Gly	1248

FIG. 6B

	Gln	_	-	_	_		-	_	_	 	1296
	gct Ala										1344
taa											1347

FIG. 6C

	1				50
DysGapC	ATGGTAGTTA	AAGTTGGTAT	TAACGGTTTC	GGTCGTATCG	GACGTCTTGC
SpyGapC					
SeqGapC					
UberGapc					
AgalGapCDNA					-t
SiniGapC				a	-t
BovGapC	~~~~~~~~~	~~~~~~~~	~~~~~~	C	-gcg-t
	51				100
DysGapC	ATTCCGTCGT	ATTCAAAATG	TTGAAGGTGT	TGAAGTAACT	CGTATCAACG
SpyGapC	c	ca	-c		t-
SeqGapC					
_					
		c-			
AgalGapCDNA	c	CC-	-a	t	
SiniGapC					t-
BovGapC	cac-a-ggc-	gc-tttt	cgcaaa	gca-cgtc	gcct-
	101				150
DysGapC	ACCTTAC	AGATCCAAAC	ATGCTTGCAC	ACTTGTTGAA	ATACGATACA
SpyGapC		t			C
SeqGapC					C
_		t			
_		tct			
AgalGapCDNA					
SiniGapC		t			t
BovGapC	cct-c-t	tc-ttc	taca-g-tct	acc-	gtt-c

FIG. 7A

```
151
                                           200
  DysGapC ACTCAAGGAC GTTTTGACGG AACTGTTGAA GTTAAAGAAG GTGGATTTGA
  SeqGapC -----a- ------ a--t---- a--t-----
UberGapc -----t- ----c--- ---a----- ----t- -----c--
SiniGapC -----t- ----c--
  BovGapC --c--ca ag--ca--- c--a--ca-g -cag-ga-c- -gaagc-c-t
        201
                                           250
  DysGapC AGTAAACGGA AACTTCATCA AAGTTTCTGC TGAACGTGAT CCAGAAAACA
   SpyGapC ---a----- ------ ------ -----t--- -----t
   SeqGapC ---a---- ------ ------ -----t--- ------
ParaUbGapC c----- --a----t- ----- ----aaa--- ----c-a-
  UberGapc ----- ----- ----- ----aaa--- -----
AgalGapCDNA -----t c-a--tg-t- ------ -----c--a ----c---
  SiniGapC ----- -g---tg-t- ----- a----c--a ----c---
   BovGapC ca-c-t--- --ggc---- cca-c-tcca g--g--a--- --t-cc----
        251
                                            300
   DysGapC TCGACTGGGC AACTGACGGT GTTGAAATCG TTCTGGAAGC AACTGGTTTC
   SpyGapC -c----- -----t--g ------ ------
   SeqGapC -c----- -----c--- ------
 ParaUbGapC -t----- ------ ------
  UberGapc -t---- -----c--- --a----- ----- -----
AgalGapCDNA -t---- t----t--c --a---- ----- -----
  SiniGapC -t----- t----t--- --a--c--- ----- ---a-----
   BovGapC -ca-g---g tga--ct--- '-c---gtat- -ag-g--gt- c----gg--
         301
   DysGapC TTTGCTAAAA AAGAAGCTGC TGAAAAACAC TTACATGCTA ACGGTGCTAA
   SpyGapC ----- ----a-- ----- -----
   ParaUbGapC ----- ---- -----t -----aa- -t-----
  UberGapc ----- ---c---- -----t ------ ------
AgalGapCDNA ----atc-- ----aaa-- --g-c---- a-c---aa- -t-----
  SiniGapC --c--tct- ---c---- ----c--- a-t--c--- ----g--
   BovGapC --ca---cc- tg--gaag-- --gggct--- --ga-g-g-. ..--c--c--
         351
                                            400
   Dysgapc AAAAGTTGTT ATCACAGCTC CTGGTGGAAA CGACGTTAAA ACAGTTGTTT
   SeqGapC --------- ------ -------
 ParaUbGapC ----- ----t---- ----g- t----g-- ----a-
   UberGapc ----- ----- -----g- t--t---- --t----a-
 AgalGapCDNA ----- ----- -----
   SiniGapC ----- ----- ----- t----- t-----
   BovGapC g-gg--ca-c ---t-t--a- --tc--...c ---t-ccccc -tgt----ga
```

FIG. 7B

```
401
                                            450
  DysGapc TCAACACTAA CCACGA.CAT TCTTGACGGT ACTGAAACAG TTATCTCAGG
  SpyGapC ----- ------
  ParaUbGapC -t----- ---t-- c----t--a ------ ----t----
  UberGapc -t----a-- ---t--.-- --a----t- -a--t----
AgalGapCDNA ----- ---- t-- c----t--a ----- -----
  SiniGapC a----- ---t--.t-- -----t--a ------ -----
  BovGapC -ggg-gtg-- ----a-g -.a-a--aac --cctc-aga --g--agcaa
        451
                                            500
  DyBGapC TGCTTCATGT ACTACAAACT GTTTAGCTCC TATGGCTAAA GCTCTTCACG
   SpyGapC ----- ---c-t--c-
   SeqGapC ----- ----- t----- t----- ---c-t--c-
 ParaUbGapC ----a---a---
  UberGapc ----- ----t---- ------ -----g----
AgalGapCDNA ----- ----a--- --c-t---- -----a----
  BovGapC ---c--c --c--c --c--- -c--g--c-- cc----c--g -tca-c--t-
         501
                                            550
   DysGapC ATGCATTTGG TATCCAAAAA GGTCTTATGA CTACAATCCA CGCTTATACT
   SpyGapC --gca--c-- -a--c--a-- ---c---- ---a----
   SeqGapC --gca---- -a--c--a-- ---c---- ---a-----
 ParaUbGapC ----- cg-a---- ---t-a--- ---a----
  UberGapc ----- -g----- ---t-g--- -a--t---- -----
AgalGapCDNA -c----- -g----- ---t-g---- ----t---- ---a----
  SiniGapC ----- -g-a----- ---t-a--- ----t---- t-g-----
   BovGapC -cc----- ca-cgtgg-g --ac---- -c--tg---- ---cat----
         551
                                             600
   DysGapC GGTGACCAAA TGATCCTTGA CGGACCACAC CGTGGTGGTG ACCTTCGTCG
   SpyGapC ----- ----- -----
   SeqGapC ----- ----g---- t----ac-gt g----- -t-----
 ParaUbGapC ----t--- --c-t---- t----t--- ----- --t-a----
  UberGapc ----- ----- ------
AgalGapCDNA ----- ------
   SiniGapC ----- --g-t---- ----- ----- ----- -t-----
   BovGapC -ccac---g- a--ctg-g-- t--c--ctc- ...--gaagc tgtgg---ga
         601
                                             650
   Dysgapc TGCTCGTGCT GGTGCTGCAA ACATTGTTCC TAACTCAACT GGTGCTGCTA
   SpyGapC ---a--C--- ------ ------ ------
   SeqGapC -----cg--
 ParaUbGapC ---c---- ----aac- -t--t---- -----
   UberGapc ----- ----aagc- ----t---- ------
AgalGapCDNA -----a -----a-
   SiniGapC ----a -c--a -c--a---
   BovGapC c-gc--a-gg -c---ccag- -t---a-c-- -gct--t--- --c---c-
```

FIG. 7C

```
651
                                                 700
   DysGapC AAGCTATCGG TCTTGTTATC CCAGAATTGA ATGGTAAACT TGATGGTGCT
   SpyGapC ----- ----- -----c-t- -c----
   SeqGapC ----- ----- ------g- -c-----
ParaUbGapC ----a---- --t----a- -t----- -----
  UberGapc ----a---- ----a-- ----a- -t----- -----
AgalGapCDNA ----- a----- a-----g- -c----- ---t----
  SiniGapC ----a---- -----a- -t----- -----
   BovGapC -g--cg-g-- caag--c-- --t--gc-c- -c--g--g-- cact--catg
         701
                                                 750
   DysGapC GCACAACGTG TTCCTGTTCC AACTGGATCA GTAACTGAGT TGGTTGTAAC
   SpyGapC -----g- ----t---
   SeqGapC -----g- ----t---
 ParaUbGapC ------ -a--a---- ---a--t--- ---a---- -a--a---gt
  UberGapc ----- -a--a--gt
AgalGapCDNA ----- ----- -----
  SiniGapC ----- -a--a--gt
   BovGapC --cttc--c- -c--cac--- c-ac-tg--t --tgtg--tc --acctgccg
         751
                                                 800
   DysGapC TCTTGATAAA AACGTTTCTG TTGACGAAAT CAACGCTGCT ATGAAAGCTG
   SpyGapC ----- a---t---- ----t-t--- ----t-t---
   SeqGapC -----t--- a---t---- ----t--- ----t
 ParaUbGapC ----a-t--- --aac---a- -a----- t---ta ------
  UberGapc ----- --aac---a- ------ ----a -----a-
AgalGapCDNA ----- ----taa--- -c----g- a--t---- ----a-
  SiniGapC ----- --tac---a- -a----- ---t----- ----a-
   BovGapC c--g--g-- cct-ccaagt a---t--g-- ---gaag-tg g----gcag-
   DysGapC CTTCAAACGA CAGTTTCGGT TACACTGAAG ATCCAATTGT TTCTTCAGAT
   SpyGapC --t----- -agc-t---- t----- t-----
   SeqGapC --t---- -agc-t---- ----- ---- t-----
 ParaUbGapC -ag-t--t-- ----at--- ----- ----- ---a--t---
  UberGapc --g----- ----a---a ------ -c----- -----t---
AgalGapCDNA -ag-t---- ----a--- --t---- ---- ---a--t---
   SiniGapC -ag-t---- ----a--- ----- --g-t---- ---a----
   BovGapC -gt--g-g-g cc-tct-aag gg--t-ct-- gctac-ct-a ggaccag-t-
          851
                                                 900
   DysGapC ATCGTAGGCG TGTCATA... CGGTTCATTG TTTGACGCAA CTCAAACTAA
   SpyGapC -----cg -a----... ------ ----c--a- -----
   SeqGapC ----cg -a----... ------ ----c--a- ------
 ParaUbGapC ----ta ----t-t... -----a --c-----
   UberGapc ---a-c--ta --g-t--... ------ ------
AgalGapCDNA ----ta -t---- ---- -----
   SiniGapC -----ta -t--t--... -----a -----a -----
   BovGapC g--tcct-cg ac-tca-cag --a-a-tcac -c-tc-a-ct tcg-tg--gg
```

					•
	901				950
DysGapC	AGTTATGGAA	GTTGACGGAT	CACAATTGGT	TAAAGTTGTA	TCATGGTATG
SpyGapC	aatggaa	t	ca	a	
			ca		
ParaUbGapC	a	t	-ta		
UberGapc	a	t	-ta		~
AgalGapCDNA	t	ct-	-c		c-
SiniGapC	a	t	-t		
BovGapC	g-ctggc-t-	-ccctcaacg	-cct	cgc-ca	cc-
	951				1000
DysGapC	ACAATGAAAT	GTCTTACACT	GCTCAACTTG	TTCGTACACT	TGAGTATTTT
SpyGapC	c			-at	c
SegGapC	c				
			a		
AgalGapCDNA			•		
_					
			aaagg		
•					
	1001	101	8		
DysGapC	GCAAAAATCG				
	t-				
_					
AgalGapCDNA					
-	~~~~~~~~~				

FIG. 7E

	1			•	50
polyGap4	MKKITGIILL	LLAVIILSAC	QANYGSGMVV	KVGINGFGRI	GRLAFRRIQN
SpyGapC					
SeqGapC	~~~~~~~~	~~~~~~~	~~~~~~		
DysGapC	~~~~~~~~	~~~~~~~~~~~	~~~~~~		
PUberGapC	~~~~~~~~~	~~~~~~~	~~~~~		
UberGapC	~~~~~~~~	~~~~~~~~	~~~~~~		
AgalGapC	~~~~~~~~~	~~~~~~~~~~	~~~~~~~		
IniaeGapC		~~~~~~~			
BovGapC	~~~~~~~~~	~~~~~~~	~~~~~~~	~~~~~~~	~~~~~~~
_					
	•				
	51				100
polyGap4	VEGVEVTRIN	DLTDPNMLAH	LLKYDTTQGR	FDGTVEVKEG	GFEVNGNFIK
DysGapC					
SpyGapC	i				
SegGapC					
PUberGapC				d-	dk
UberGapC				d-	
AgalGapC					q-v-
IniaeGapC				d-	g-v-

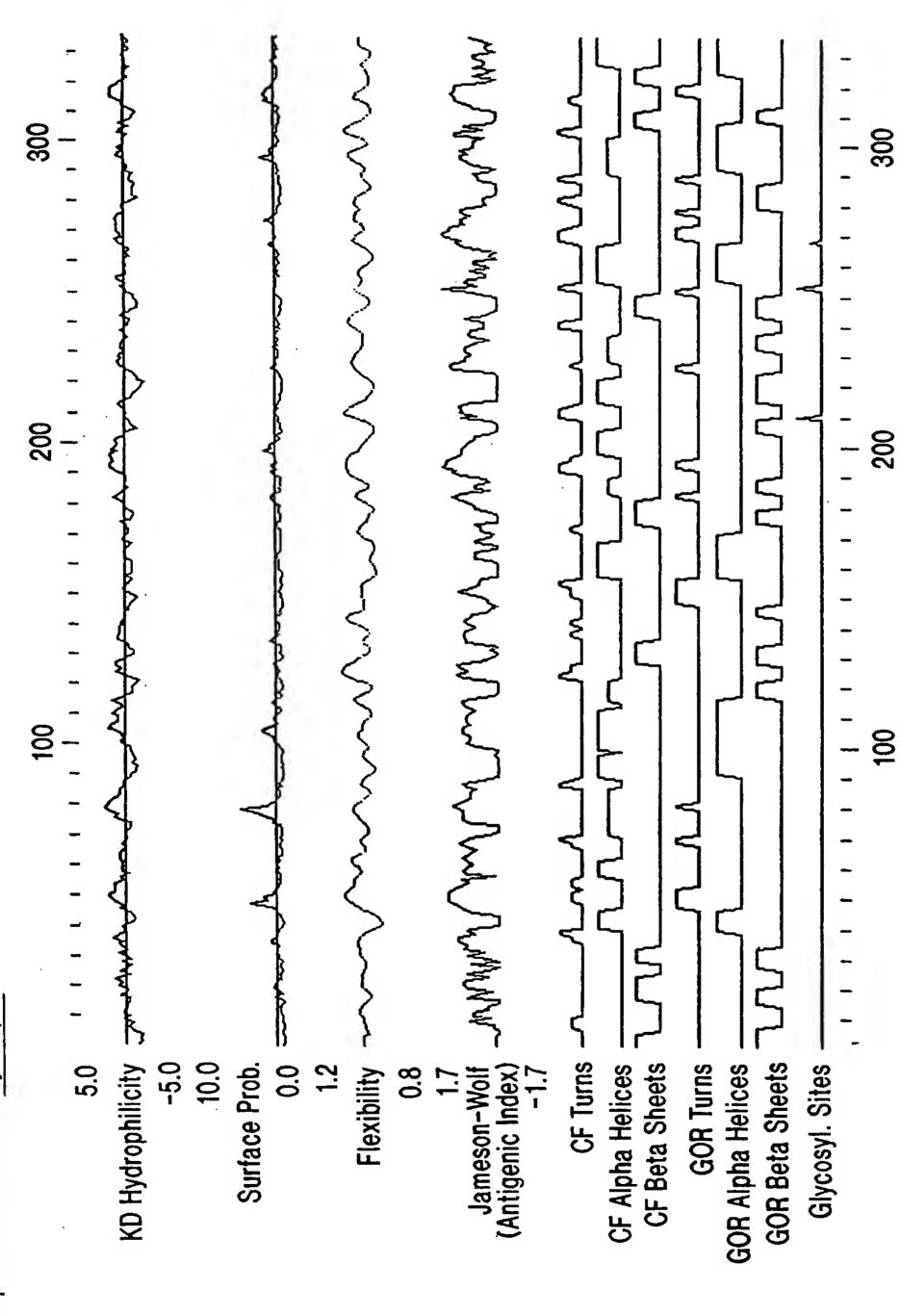
FIG. 8A

	101				150
	VSAERDPENI			•	
DysGapC		• • • • • • • • •	• • • • • • • • • •	• • • • • • • • •	• • • • • • • • • •
SpyGapC		• • • • • • • • •	• • • • • • • • • • •	• • • • • • • • •	• • • • • • • • •
SeqGapC		• • • • • • • • •	• • • • • • • • •	• • • • • • • • •	• • • • • • • • • •
PUberGapC	k	• • • • • • • • •		• • • • • • • • •	• • • • • • • • • •
UberGapC	k	• • • • • • • • • • •	• • • • • • • • • •	• • • • • • • • •	• • • • • • • • •
AgalGapC	e-a	• • • • • • • • • •	• • • • • • • • • •	• • • • • • • • •	• • • • • • • • •
IniaeGapC	e-a	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • •	• • • • • • • • • •	• • • • • • • • •
BovGapC	~~~~~~~~~	~~~~~~~~~~	rigrl-tr	aafnsgkvdi	vaindpfi-l
	151				200
			EVKEGGFEVN		
DysGapC	• • • • • • • • •	• • • • • • • • • •		• • • • • • • • • •	
SpyGapC	• • • • • • • • •	• • • • • • • • •	• • • • • • • • •	• • • • • • • • • •	
SeqGapC	• • • • • • • • •	• • • • • • • • •		• • • • • • • • • •	
PUberGapC	• • • • • • • • •	• • • • • • • • •		• • • • • • • • • • • • • • • • • • • •	q
UberGapC	• • • • • • • • •	• • • • • • • • •		• • • • • • • • • • • • • • • • • • • •	
AgalGapC	• • • • • • • • •	• • • • • • • • •	• • • • • • • •	• • • • • • • • • •	
IniaeGapC	• • • • • • • • •	• • • • • • • • •	• • • • • • • •	• • • • • • • • •	
BovGapC	hymvymfqyd	sthgkfn	kaen-klvi-	-kaitifq	dk-gda
polyGap4	201 GVEIVLEATS	FFAKKEAAEK	HLHANGAKKV	VITAPGGNDV	250 KTVVFNTNHD
polyGap4 DysGapC	GVEIVLEATS	FFAKKEAAEK	HLHANGAKKV	VITAPGGNDV	KTVVFNTNHD
polyGap4 DysGapC SpyGapC	GVEIVLEATS	FFAKKEAAEK	HLHANGAKKV	VITAPGGNDV	KTVVFNTNHD
DysGapC SpyGapC SeqGapC	GVEIVLEATS		p		KTVVFNTNHDqlfstltts
DysGapC SpyGapC SeqGapC	GVEIVLEATS				KTVVFNTNHDqlfstltts
DysGapC SpyGapC SeqGapC PUberGapC	GVEIVLEATS	a	p	d	KTVVFNTNHDqlfstltts
DysGapC SpyGapC SeqGapC PUberGapC UberGapC	GVEIVLEATS	a	p	d	KTVVFNTNHDqlfstltts
DysGapC SpyGapC SeqGapC PUberGapC UberGapC AgalGapC	GVEIVLEATS	a a sk-gq	p	d	KTVVFNTNHDqlfstltts
DysGapC SpyGapC SeqGapC PUberGapC UberGapC AgalGapC IniaeGapC	GVEIVLEATS	a sk-gq s-aq	p	d	KTVVFNTNHD
DysGapC SpyGapC SeqGapC PUberGapC UberGapC AgalGapC IniaeGapC	GVEIVLEATS	a sk-gq s-aq	p	d	KTVVFNTNHD
DysGapC SpyGapC SeqGapC PUberGapC UberGapC AgalGapC IniaeGapC	GVEIVLEATS	a sk-gq s-aq	p	d	KTVVFNTNHD
DysGapC SpyGapC SeqGapC PUberGapC UberGapC AgalGapC AgalGapC IniaeGapC BovGapC	GVEIVLEATS	a a sk-gq s-aq v-ttm-k-ga	p	i-ssaa	KTVVFNTNHDqlfstlttsy pmf-mgve
DysGapC SpyGapC SeqGapC PUberGapC UberGapC AgalGapC AgalGapC IniaeGapC BovGapC	GVEIVLEATS	a sk-gq s-aq v-ttm-k-ga	p	i-ssaa	KTVVFNTNHDqlfstlttsy pmf-mgve
DysGapC SpyGapC SeqGapC PUberGapC UberGapC AgalGapC AgalGapC IniaeGapC BovGapC PolyGap4 DysGapC SpyGapC	GVEIVLEATS	a sk-gq s-aq v-ttm-k-ga	p	i-ssaa	TOTAL STATE OF THE
DysGapC SpyGapC SeqGapC PUberGapC UberGapC AgalGapC AgalGapC IniaeGapC BovGapC PolyGap4 DysGapC SpyGapC	GVEIVLEATS	GASCTINCLA	p	i-ssaa	TVVFNTNHD
DysGapC SpyGapC SeqGapC PUberGapC UberGapC AgalGapC AgalGapC IniaeGapC BovGapC PolyGap4 DysGapC SpyGapC	GVEIVLEATS	GASCTINCLA	p	i-ssaa	TVVFNTNHD
DysGapC SpyGapC SeqGapC PUberGapC UberGapC AgalGapC AgalGapC IniaeGapC BovGapC PolyGap4 DysGapC SpyGapC SeqGapC PUberGapC UberGapC	GVEIVLEATS	GASCTINCLA	p	GIQKGLMTTIvkq	TTVVFNTNHD
DysGapC SpyGapC SeqGapC PUberGapC UberGapC AgalGapC AgalGapC IniaeGapC BovGapC PolyGap4 DysGapC SpyGapC SeqGapC PUberGapC UberGapC	GVEIVLEATS	GASCTINCLA	p	GIQKGLMTTIvkq	TTVVFNTNHD
DysGapC SpyGapC SeqGapC PUberGapC UberGapC AgalGapC IniaeGapC BovGapC PolyGap4 DysGapC SpyGapC SpyGapC SeqGapC PUberGapC UberGapC AgalGapC	GVEIVLEATS	GASCTTNCLA	p	GIQKGLMTTI	TVVFNTNHD
DysGapC SpyGapC SeqGapC PUberGapC UberGapC AgalGapC IniaeGapC BovGapC PolyGap4 DysGapC SpyGapC SeqGapC PUberGapC UberGapC UberGapC AgalGapC IniaeGapC	GVEIVLEATS	GASCTINCLA	p	GIQKGLMTTI	TVVFNTNHD

```
polygap4 DGPHRGGDLR RARAGAANIV PNSTGAAKAI GLVIPELNGK LDGAAQRVPV
 DysGapC ----- ----- -----
 SpyGapC ----- -----
 SeqGapC --hrg---- ------ ----r--- ------
PUberGapC ----- ----n--- ------ -----
UberGapC ----- ----s--- ------
AgalGapC ----- ----- ----- ----- -----
IniaeGapC ----- ---a---- ---- ----- -----
 BovGapC ---.s-klw- dg-ga-q--i -a----v -k----- -t-m-f---t
       351
                                             400
polyGap4 PTGSVTELVV TLDKNVSVDE INAAMKAASN DS....FGYT EDPIVSSDIV
 DysGapC ----- ----- ------ ------
 SpyGapC ----- ----- ----- -----
 SeqGapC ----- ----- ----- ----- -----
PUberGapC ----a v-n-et--e- --sv---a- --...y--- ------
 UberGapC -----a v-e-et--e- ----a- --...y--- -----i
 AgalGapC -----a --e-d-t-e- v----a- --...y--- ------
IniaeGapC -----a v-e-dt--e- ----a- --...y--- --a-----
 BovGapC -nv--vd-tc r-e-paky-- -kkvv-q--e gplkgil--- --qv--c-fn
                                              450
        401
 polyGap4 GVSYGSLFDA TQTKVMEVDG SQLVKVVSWY DNEMSYTAQL VRTLEYFAKI
  SpyGapC ----- ----- ----- -----
  SeqGapC ----- ------ ------
PUberGapC -m-f----- ----qt--- n----- ----- d------
 UberGapC -ma----- ----qt--- n-----
 AgalGapC -i----- ----qt--- n----- -----s-- -----s--
IniaeGapC -i----- ----qt --- n----- ----- -----
  BovGapC sdths-t--- gagial...n dhf--li--- ---fg-sk-~ ~~~~~~~
        451
 polyGap4 AK
  DysGapC --
  SpyGapC --
  SegGapC --
 PUberGapC --
 UberGapC --
 AgalGapC --
 IniaeGapC --
  BovGapC ~~
```

350

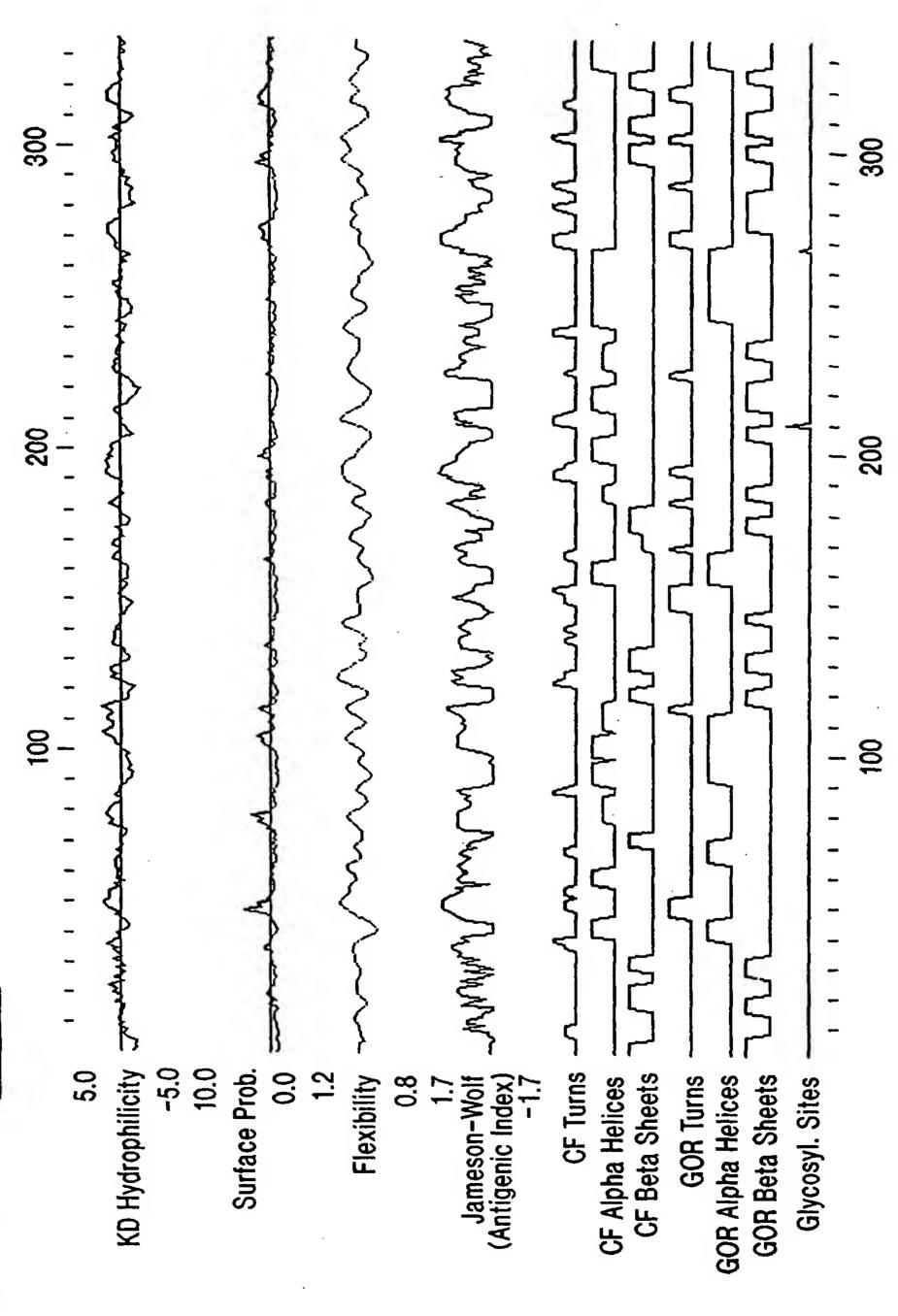
FIG. 8C



<u>ඩ</u> ග

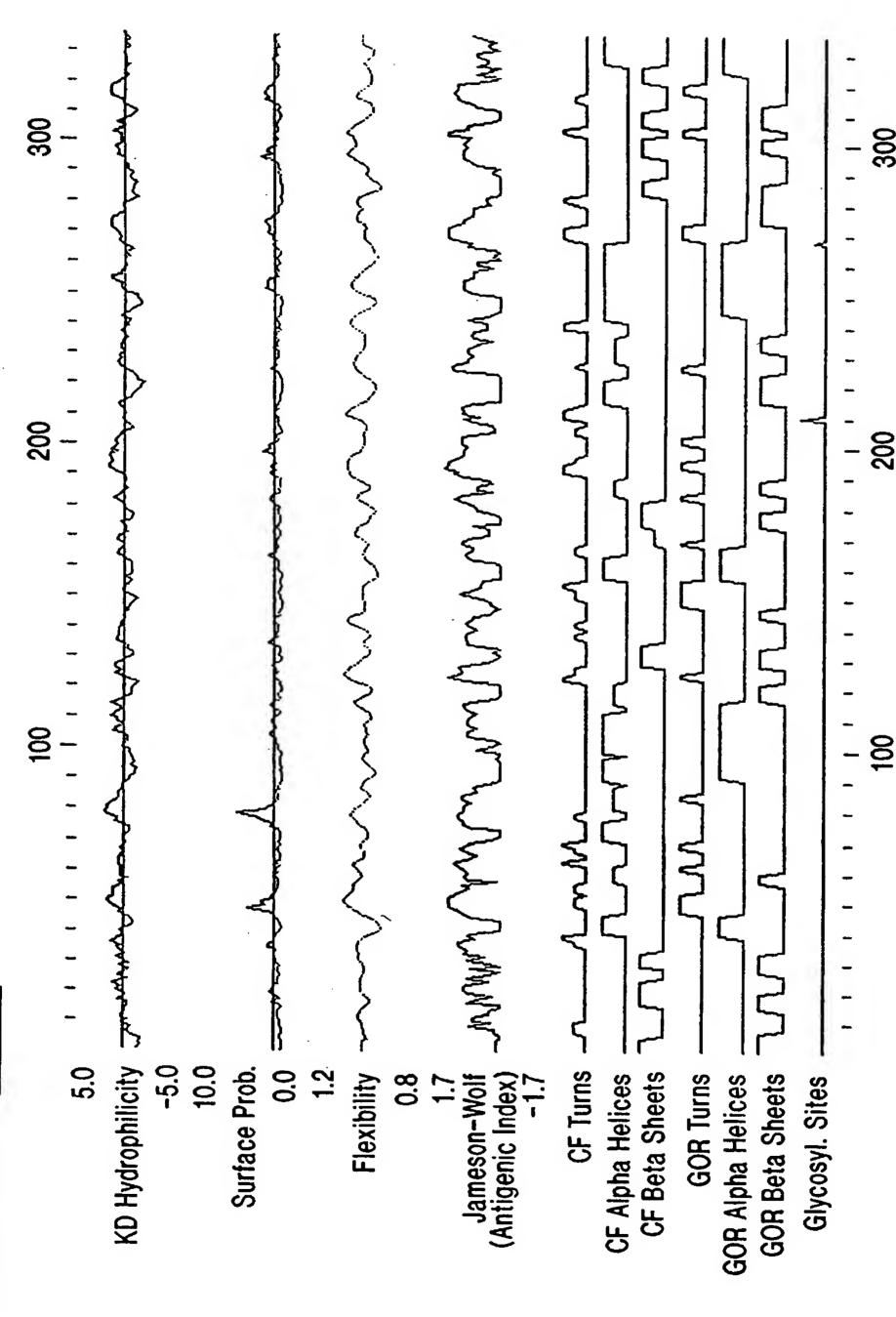
Peptide Structure Results

Peptide Structure of: AgalGapC









Peptide Structure Results

Peptide Structure of: PUberGapC

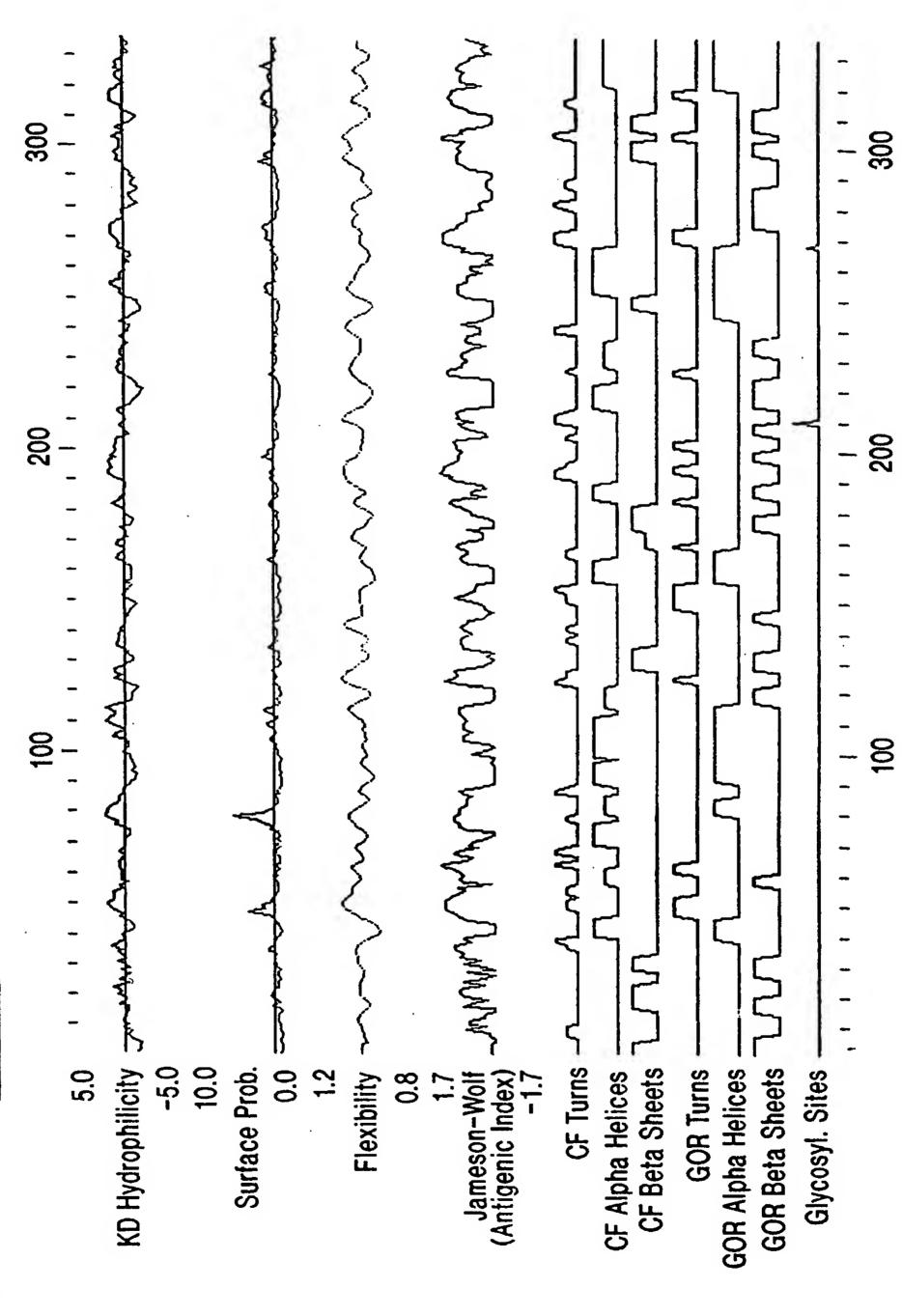
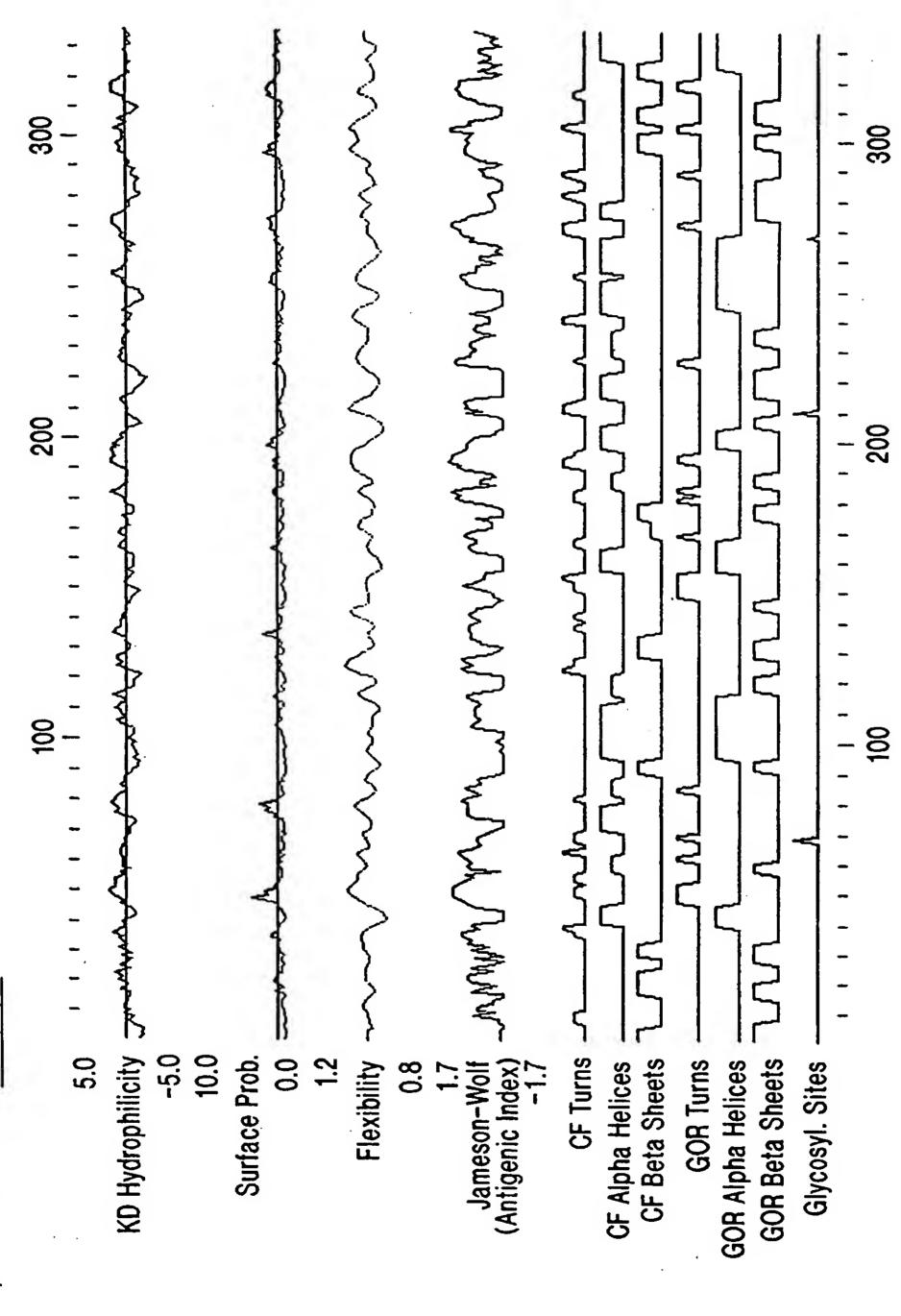


FIG. 12



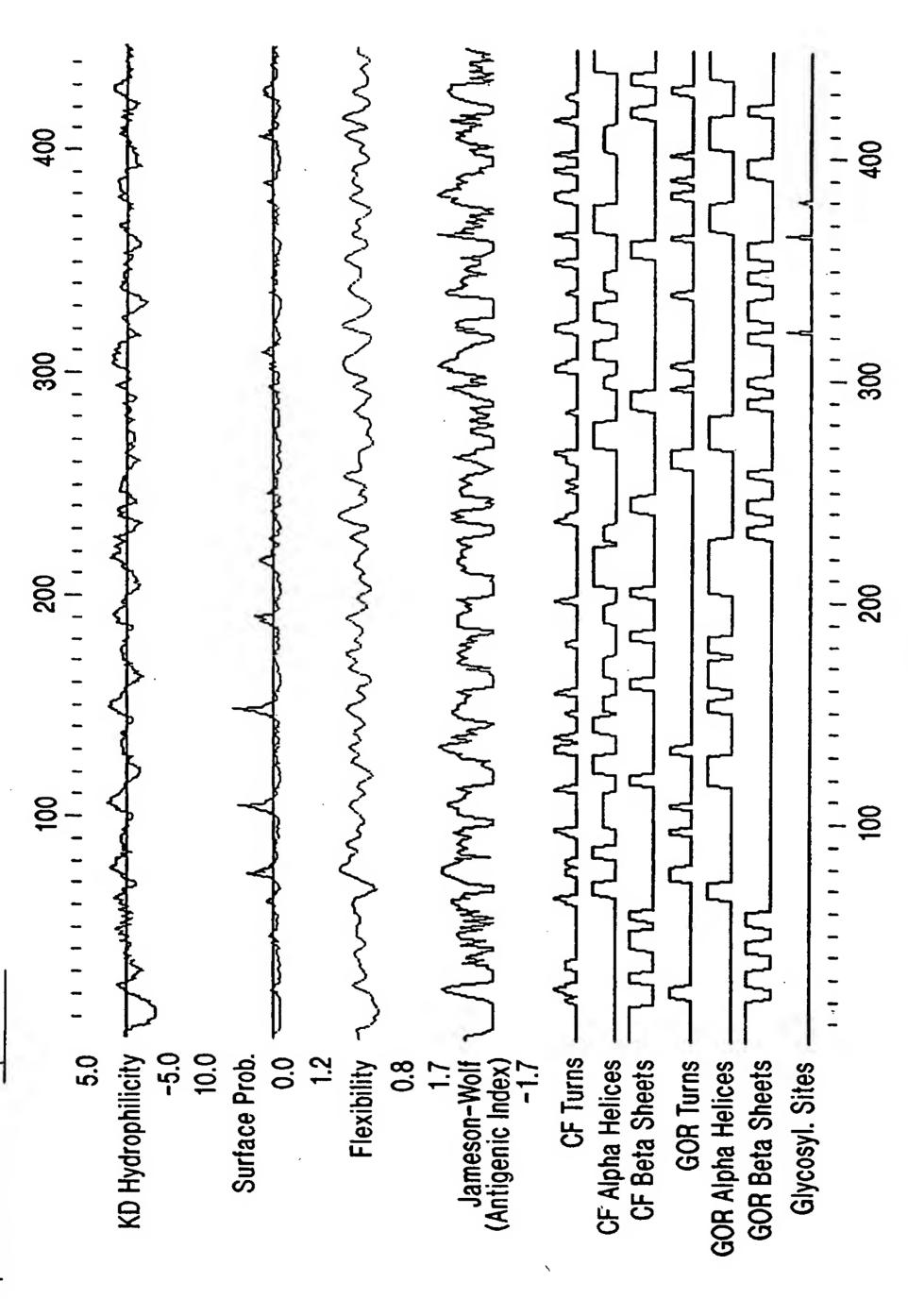
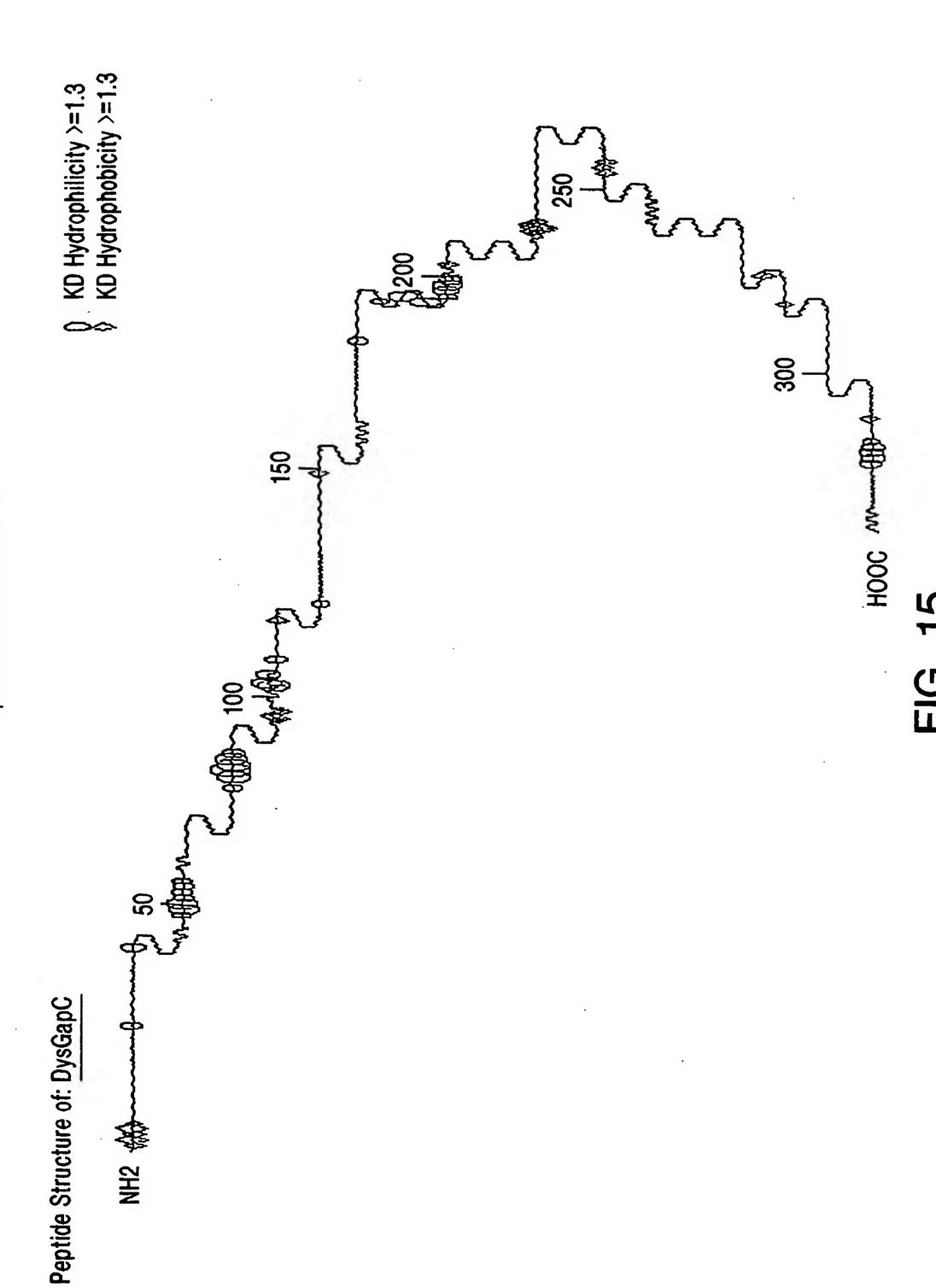


FIG. 14



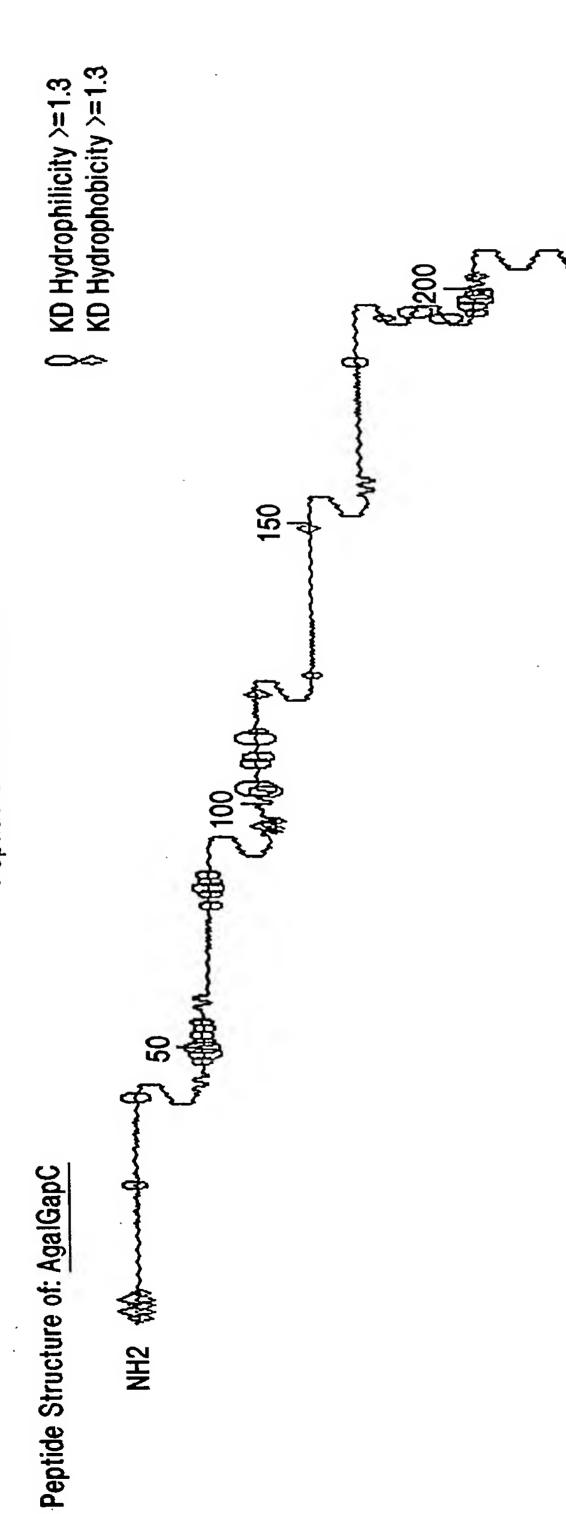


FIG. 16

HOOC Wy

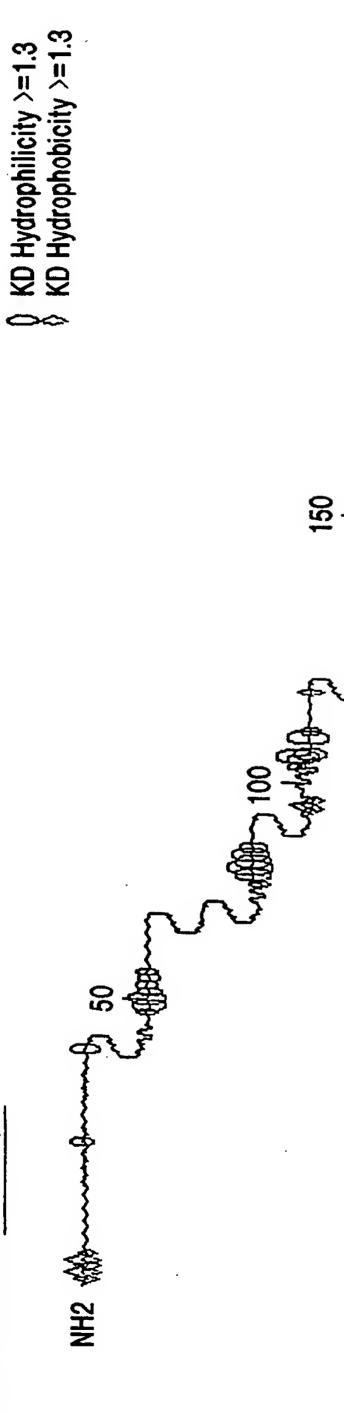
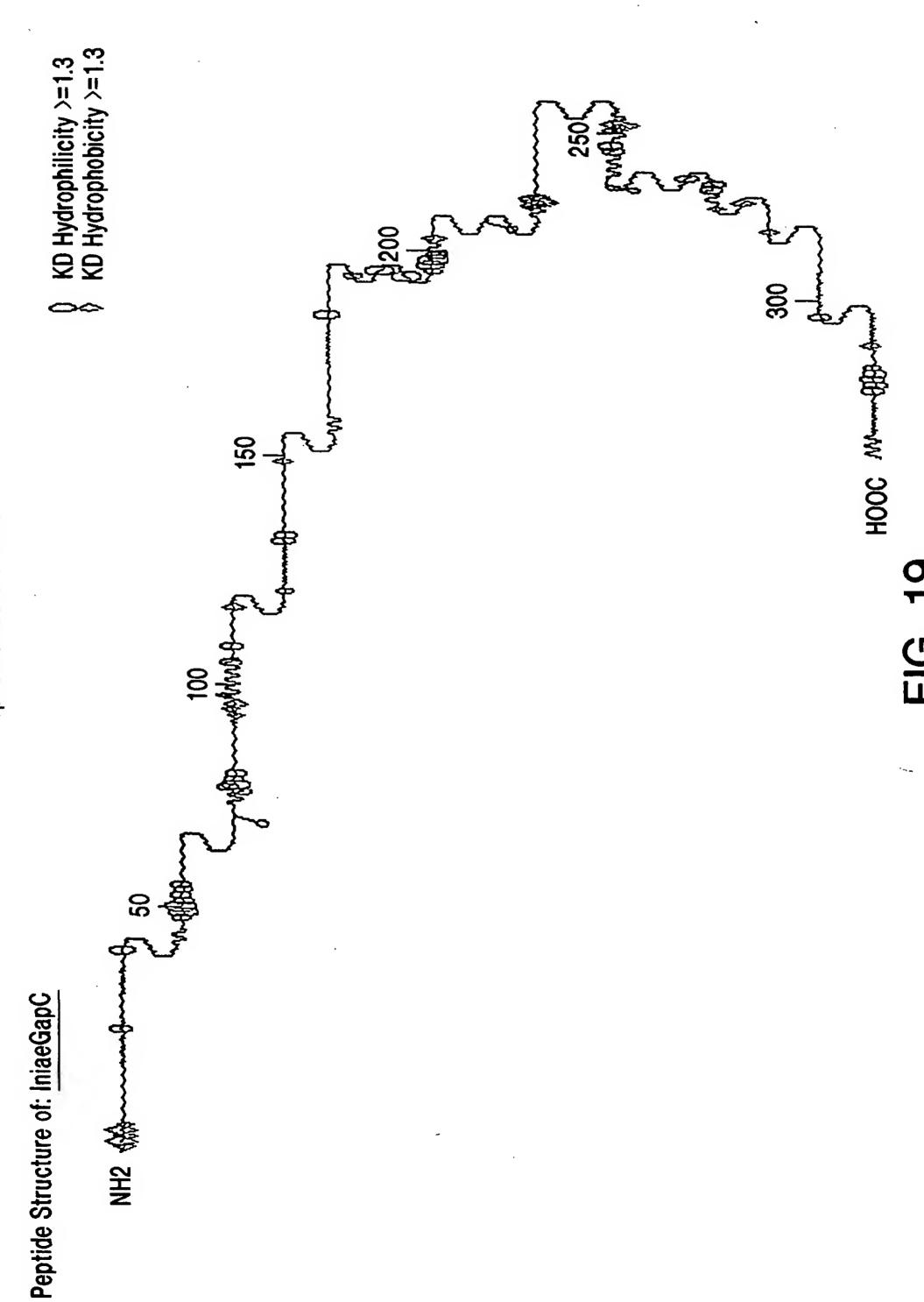


FIG. 18

H00C



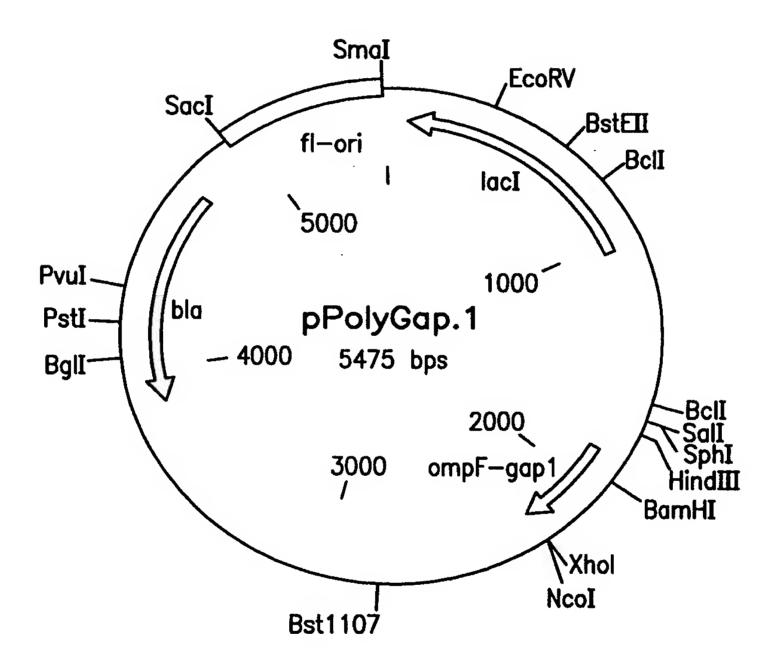


FIG. 21

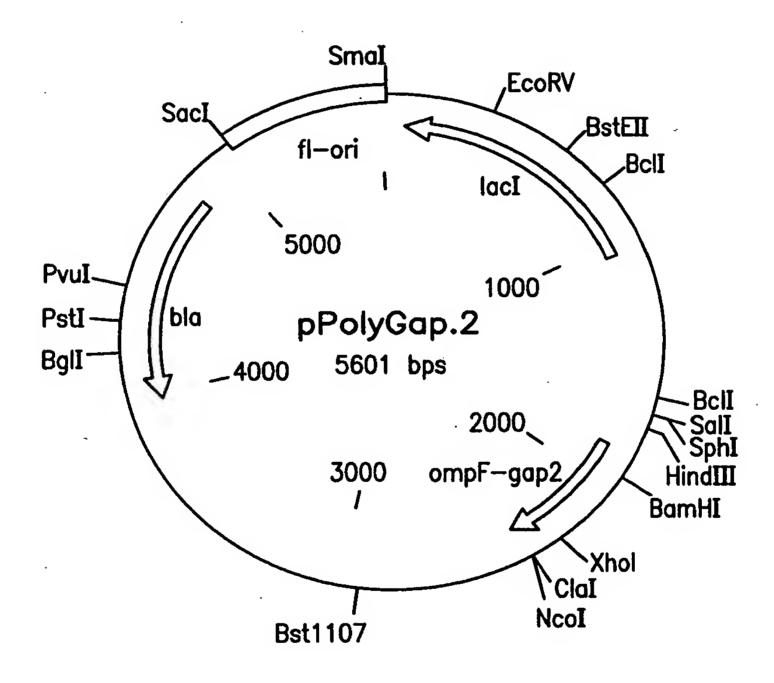


FIG. 22

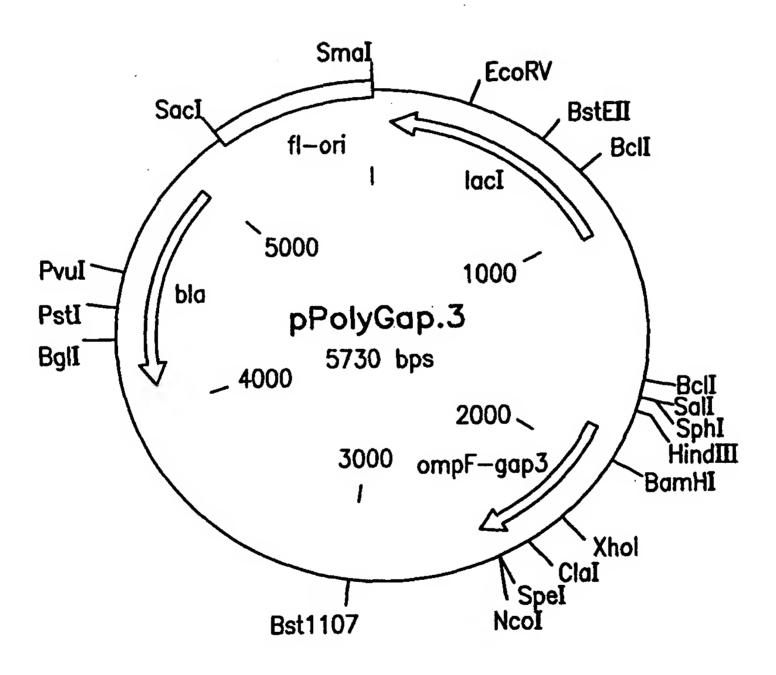


FIG. 23

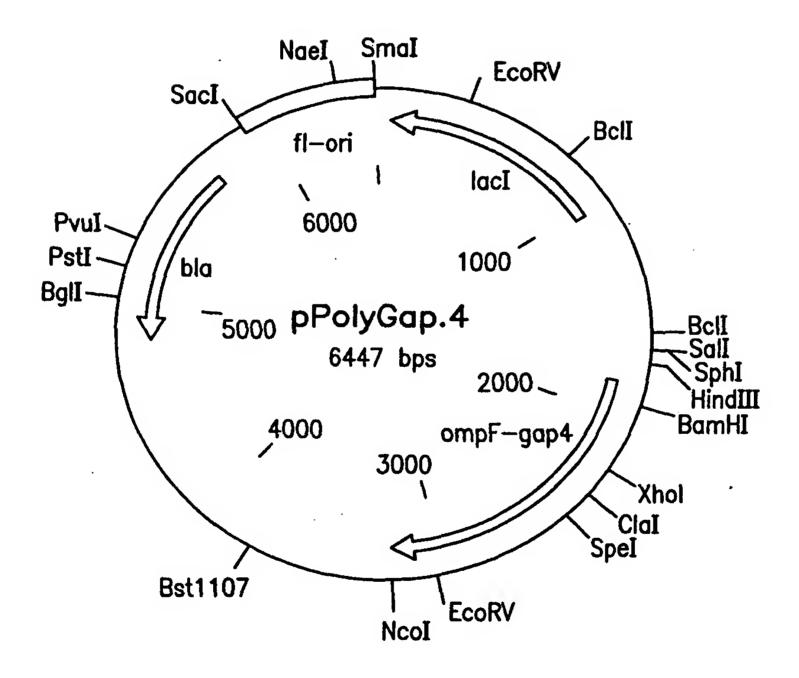


FIG. 24

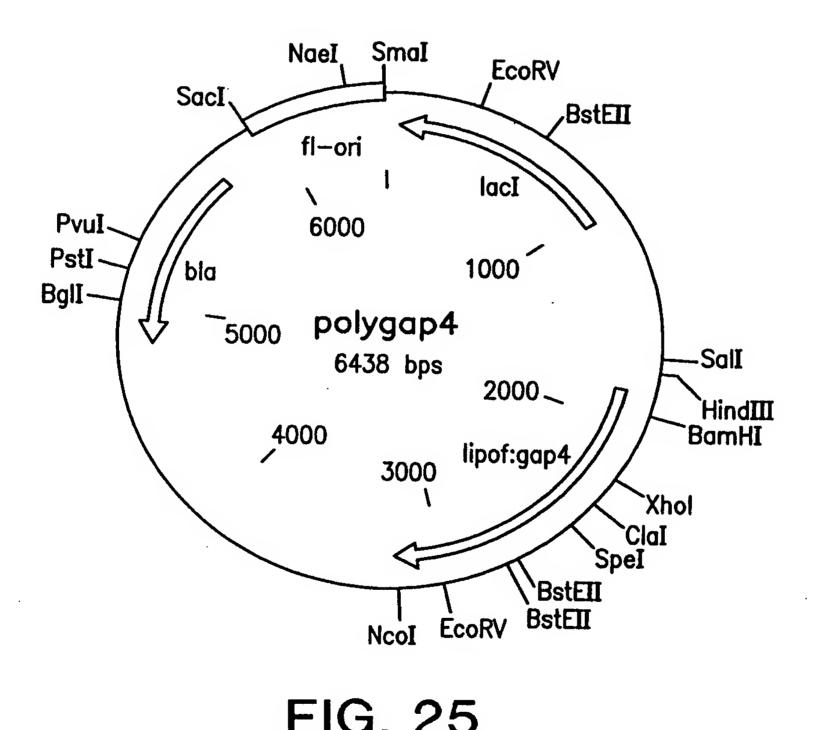


FIG. 25